

WORLD INTELLECTUAL PROPERTY ORGANIZATION International Bureau



INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

WO 93/08300 (51) International Patent Classification 5: (11) International Publication Number: **A1** C12P 21/06 (43) International Publication Date: 29 April 1993 (29.04.93) (74) Agent: DILLAHUNTY, T., Gene; Burns, Doane, Swecker & Mathis, George Mason Building, Washington and Prince Streets, P.O. Box 1404, Alexandria, VA PCT/US92/08881 (21) International Application Number: 16 October 1992 (16.10.92) (22) International Filing Date: 22313-1404 (US). (30) Priority data: (81) Designated States: CA, JP, European patent (AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, SE). US 18 October 1991 (18.10.91) 777,709 (71) Applicant: THE UNIVERSITY OF CALGARY [CA/CA]; **Published** 2500 University Drive, N.W., Calgary, Alberta T2N 1N4 With international search report. (71)(72) Applicants and Inventors: NG, Shi, Chung [GB/US]; 6
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(54) Title: EXPRESSION-SECRETION VECTORS FOR THE PRODUCTION OF BIOLOGICALLY ACTIVE FV FRAGMENTS

(57) Abstract

Expression-secretion vectors capable of producing biologically active Fv fragments or single chain Fv molecules, host cells containing these expression-secretion vectors, and methods for producing biologically active Fv fragments or single chain Fv molecules.

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EXPRESSION-SECRETION VECTORS FOR THE PRODUCTION OF BIOLOGICALLY ACTIVE FV FRAGMENTS

BACKGROUND OF THE INVENTION

The Fv fragment is the smallest complete antigen binding site presently known. This fragment is composed of only the variable domains of the immunoglobulin variable heavy (V_{μ}) and variable light (V_{I.}) chains. The small size of the 10 Fv fragment has generated a great deal of interest in the antibody and protein engineering fields because of its potential application in imaging, therapeutics, and structural studies. Initial attempts to generate Fv were made using proteolytic 15 cleavage of whole antibody. However, this technique was hindered by difficulties in controlling both quality and yield (Inbar et al., Proc. Natl. Acad. Sci. USA 69, 2659 [1972]). Recombinant DNA techniques were later employed in 20 attempts to express native Fv in bacterial cells. Some groups have tried to express the individual $\mathbf{v}_{_{\mathbf{H}}}$ and $\mathbf{v}_{_{\mathbf{L}}}$ chains and reassociate the chains in vitro. The production of these proteins intracellularly resulted in insoluble proteins which had 25 to be denatured and renatured to generate functional antibody. It is not clear what the exposure to

denaturants will do to native antibody structure

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and hence these systems are less than ideal. More recently, the production of soluble native Fv (Skerra and Pluckthun, Science 240, 1038 [1988]) and other related fragments (Better et al., Science 240, 1041 [1988]) has been reported. However, the yields of native Fv reported in these systems are quite low (0.2 mg/liter of cells) for many practical applications (e.g., isotope labeling for 3-D NMR analysis).

It would be useful to have improved expression-secretion systems for the production of biologically active Fv fragments and single chain Fv molecules.

SUMMARY OF THE INVENTION

The present invention concerns expressionsecretion systems for the production of biologically active Fv fragments and single chain Fv molecules.

In particular, the present invention concerns an expression-secretion vector capable of producing a biologically active Fv fragment comprising a DNA sequence encoding the T7 promoter, a DNA sequence encoding the variable domain of an immunoglobulin heavy chain (V_H) , a DNA sequence encoding the variable domain of an immunoglobulin light chain (V_L) , and one or more DNA sequences encoding one or more signal peptide sequences.

The present invention further concerns a host cell containing an expression-secretion vector capable of producing a biologically active Fv fragment comprising a DNA sequence encoding the T7 promoter, a DNA sequence encoding the variable domain of an immunoglobulin heavy chain, a DNA

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sequence encoding the variable domain of an immunoglobulin light chain, and one or more DNA sequences encoding one or more signal peptide sequences.

The present invention additionally concerns a method for producing a biologically active FV fragment comprising culturing a host cell containing an expression-secretion vector capable of producing a biologically active FV fragment which comprises a DNA sequence encoding the T7 promoter, a DNA sequence encoding the variable domain of an immunoglobulin heavy chain, a DNA sequence encoding the variable domain of an immunoglobulin light chain, and one or more DNA sequences encoding one or more signal peptide sequences under conditions permitting expression-secretion of the biologically active FV fragments.

The present invention also concerns an expression-secretion vector capable of producing a biologically active single chain Fv (sFv) molecule comprising a DNA sequence encoding the T7 promoter, a DNA sequence encoding a single chain Fv molecule, and a DNA sequence encoding a signal peptide sequence.

25 BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 shows the nucleotide and deduced amino acid sequences of the (A) $\rm V_H$ [SEQ. ID NO. 1] and (B) $\rm V_L$ [SEQ. ID NO. 2] portions of antidigoxin monoclonal antibody 26-10. Restriction sites are shown.

Figure 2 shows the modified DNA sequences encoding and the deduced amino acid sequences of the signal peptide sequences (A) ompA [SEQ. ID NO. 3]

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and (B) phoA [SEQ. ID NO. 4]. Arrows indicate the change of nucleotides at these particular positions to generate desirable restriction enzyme recognition sites.

Figure 3 shows the various plasmids produced in generating plasmid FvpD: (A) Construction of plasmid V_HpD; (B) Construction of plasmid V_TpD; (C) Construction of plasmid V_LpD-Xbal; (D) Construction of plasmid FvpD.

Figure 4 is a sodium dodecyl sulphate (SDS) polyacrylamide gel demonstrating the production of the 26-10 Fv fragment. Lanes 1-4: Eluted fraction numbers 3 to 6 from ouabain column. Peak of Fv is at fraction 3. Lane 5: Protein size standards 16.9, 14.4, 8.2 kd. Lane 6: Prestained protein 15 size standards 110, 84, 47, 33, 24, 16 kd. Lane 7: Fv periplasmic fraction before column purification. Figure 5 shows the constructs of plasmid pT7PhoA 26-10sFv.

Figure 5 shows the construction of plasmid pT7PhoA26-10sFv.

Figure 6 shows the DNA sequence encoding and the amino acid sequence of the 26-10 single chain Fv molecule. Restriction sites and some 5' and 3' non-coding sequences are shown.

DETAILED DESCRIPTION OF THE INVENTION

The present invention concerns an expressionsecretion vector capable of producing a biologically active Fv fragment comprising a DNA sequence encoding the T7 promoter, a DNA sequence encoding the variable domain of an immunoglobulin heavy chain, a DNA sequence encoding the variable domain of a immunoglobulin light chain, and one or more DNA sequences encoding one or more signal peptide

The present invention also concerns an seguences. expression-secretion vector capable of producing a biologically active single chain Fv (sFv) molecule comprising of DNA sequence encoding the T7 promoter, a DNA sequence encoding a single chain . Fy molecule, and a DNA sequence encoding a signal peptide sequence. Preferably, the biologically active Fv fragment or sFv molecule has authentic N-termini (i.e., the mature Fv fragment or sFv molecule is generated by cleavage of the peptide 10 bond between the carboxy terminus of the signal peptide sequence and the amino terminus of the variable domain of the immunoglobulin heavy or light chain). Further preferred are expressionsecretion vectors wherein the signal peptide 15 sequences are ompA and phoA. Additionally preferred are expression-secretion vectors wherein the DNA sequences encoding the signal peptide sequences have been modified to generate additional restriction enzyme sites without changing the amino 20 acid sequences of the signal peptide sequences. Also preferred is an expression-secretion vector capable of producing a biologically active Fv fragment comprising a DNA sequence encoding the T7 promoter operatively 25 linked to a DNA sequence encoding the variable domain of an immunoglobulin heavy chain, a DNA sequence encoding the variable domain of an immunoglobulin light chain, and one or more DNA sequences

As used in this context, the term "operatively linked" means that the T7 promoter is capable of directing the transcription of the DNA

encoding one or more signal peptide sequences.

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sequences encoding the variable domains of the immunoglobulin heavy and light chains.

As used in the present application, the term "Fv fragment" means the non-covalently associated variable domains of the immunoglobulin heavy and light chains which can bind antigen but which lack the effector functions of the constant regions of the immunoglobulin heavy and light chains.

As used in the present specification, the term "single chain Fv molecule" means a molecule in which variable domains of the immunoglobulin heavy and light chains which can bind antigen but which lack effector functions of the constant regions of the immunoglobulin heavy and light chains are joined using an amino acid linker.

As used in the present specification, the terms "biologically active Fv fragment" or "biologically active sFv molecule" means that the Fv fragment or sFv molecule is capable of specifically binding one or more of the same antigens as the full length antibody from which it is derived.

Expression-secretion vectors of utility in the present invention are often in the form of "plasmids", which refer to circular double stranded DNAs which, in their vector form, are not bound to the chromosome. However, the invention is intended to include such other forms of expression-secretion vectors which serve equivalent functions and which become known in the art subsequently hereto.

The expression-secretion vectors of the present invention capable of producing a biologically active Fv fragment at a minimum contain a DNA sequence encoding the T7 promoter, a

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DNA sequence encoding the variable domain of an immunoglobulin heavy chain, a DNA sequence encoding the variable domain of an immunoglobulin light chain, one or more DNA sequences encoding one or more signal peptides sequences (e.g., ompA, 5 phoA, pelB) and the remaining vector. expression-secretion vectors of the present invention capable of producing a biologically active sFv molecule at a minimum contain a DNA sequence encoding a T7 promoter, a DNA sequence 10 encoding a single chain Fv molecule, a DNA sequence encoding a signal peptide sequence and the remaining vector. ompA and phoA are signal peptide sequences which are encoded by DNA sequences identical to or derived from the Escherichia coli 15 (E. coli) ompA and phoA loci. The ompA locus is the structural gene for an E. coli outer membrane protein, and the phoA locus is the structural gene of E. coli alkaline phosphatase. The remaining vector must, of course, contain an origin of 20 replication, for example, a colEI origin of replication. The expression-secretion vectors may also include other DNA sequences known in the art, for example, stability leader sequences which provide for stability of the plasmid, transcription 25 termination sequences, regulatory sequences which allow expression-secretion of the structural gene to be modulated (e.g., by the presence or absence of nutrients or other inducers in the growth medium), marker sequences (e.g., for ampicillin and 30 kanamycin resistance) which are capable of providing phenotypic selection in transformed host cells, and sequences which provide sites for

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cleavage by restriction endonucleases. The characteristics of the actual expression-secretion vector used must be compatible with the host cell which is to be employed. For example, when cloning in a bacterial system, the expression-secretion vector should contain DNA sequence (e.g., the T7 promoter) capable of functioning in that system. An expression-secretion vector as contemplated by the present invention is capable of directing the replication and the expression of DNA sequences encoding the variable domains of the immunoglobulin heavy and light chains or single chain Fv molecules.

Particularly preferred are the expression-secretion vectors designated FvpD or pT7PhoA 26-10sFv, described herein below, or expression-secretion vectors with the identifying characteristics of FvpD or pT7PhoA26-10sFv.

Suitable expression-secretion vectors containing the desired coding and control sequences may be constructed using standard recombinant DNA techniques known in the art, many of which are described in Maniatis, T. et al., Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY (1982).

Of course, an integral component of the expression-secretion vectors of the present invention are DNA sequences coding for immuno-globulin $\mathbf{V}_{\mathbf{H}}$ and $\mathbf{V}_{\mathbf{L}}$ chains or for single chain Fv molecules. Such DNA sequences can be generated in various ways. In one approach, the DNA sequences of the present invention coding for immunoglobulin $\mathbf{V}_{\mathbf{H}}$ and $\mathbf{V}_{\mathbf{L}}$ chains or for single chain Fv molecules

can be chemically synthesized. For example, DNA sequences coding for immunoglobulin $V_{\rm H}$ and $V_{\rm L}$ chains or for single chain Fv molecules can be synthesized as a series of 100 base oligonucleotides that can then be sequentially ligated (via appropriate terminal restriction sites) so as to form the correct linear sequence of nucleotides [on the condition that the nucleotide sequences of the $V_{\rm H}$ and $V_{\rm L}$ chains or single chain Fv molecules are known].

In a second approach, DNA sequences coding for immunoglobulin $V_{\rm H}$ and $V_{\rm L}$ chains or for single chain Fv molecules can be generated using polymerase chain reaction (PCR).

Briefly, pairs of synthetic DNA oligonucleotides at 15 least 15 bases in length (PCR primers) that hybridize to opposite strands of the target (template) DNA sequence are used to enzymatically amplify the intervening region of DNA on the target sequence. Suitable template DNA sequences may be 20 generated, for example, by isolating mRNA from a hybridoma of interest and reverse transcribing the Suitable PCR primers may be chemically synthesized, and may be designed by sequencing mRNA from a hybridoma of interest, by sequencing the 25 antibody molecule itself and producing degenerate primers, or by using generic primers [See, Orlandi et al., Proc. Natl. Acad. Sci. USA <u>86</u>, 3833 (1989); Sastry et al., Proc. Natl. Acad. Sci. USA 86, 5728 (1989)]. Suitable 5' primers include, for example, 30 those based on mature termini of the immunoglobulin ${
m V}_{
m H}$ and ${
m V}_{
m L}$ chains, and suitable 3' primers include,

for example, those based on the heavy and light

chain J regions. Repeated cycles of heat denaturation of the template, annealing of the primers and extension of the 3'-termini of the annealed primers with a DNA polymerase results in amplification of the segment defined by the 5' ends of the PCR primers. See, U.S. Patent Nos. 4,683,195 and 4,683,202.

The present invention further concerns a host cell containing an expression-secretion vector capable of producing a biologically active Fv 10 fragment comprising a DNA sequence encoding the T7 promoter, a DNA sequence encoding the variable domain of an immunoglobulin heavy chain, a DNA sequence encoding the variable domain of an immunoglobulin light chain, and one or more DNA sequences 15 encoding one or more signal peptide sequences. The present invention also concerns a host cell containing an expression vector capable of producing a biologically active single chain Fv molecule comprising a DNA sequence encoding a T7 20 promoter, a DNA sequence encoding a single chain Fy molecule and a DNA sequence encoding a signal peptide sequence. Preferably, the biologically active Fv fragment or single chain Fv molecule has authentic N-termini (i.e., the mature Fv 25 fragment or single chain Fv molecule is generated by cleavage of the peptide bond between the carboxy terminus of the signal peptide sequence and the amino terminus of the variable domain of the immunoglobulin heavy or light chain). Further 30 preferred are expression-secretion vectors wherein the signal peptide sequences are ompA and phoA. Additionally preferred are expression-secretion

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vectors wherein the DNA sequences encoding the signal peptide sequences have been modified to generate additional restriction enzyme sites without changing the amino acid sequences of the signal peptide sequences. Also preferred are host cells containing an expression-secretion vector capable of producing a biologically active Fv fragment comprising a DNA sequence encoding the T7 promoter operatively linked to a DNA sequence encoding the variable domain of an immunoglobulin heavy chain, a DNA sequence encoding the variable domain of an immunoglobulin light chain, and one or more DNA sequences encoding one or more signal peptide sequences.

Suitable host cells include Escherichia colicells, such as Escherichia coli MC1061 cells.

Other suitable E. coli strains include GM-1,
SG-935 and 1023. Particularly preferred host
cells are those containing an integrated copy of the T7 RNA polymerase gene, such as E. coli strains
JM109/DE3 and BL21/DE3/pLysS.

The expression-secretion vectors of the present invention may be introduced into host cells by various methods known in the art. For example, transformation of host cells with expression-secretion vectors can be carried out as described in Maniatis et al., supra. However, other methods for introducing expression-secretion vectors into host cells, for example, electroporation, liposomal fusion, or viral or phage infection can also be employed.

Host cells producing active Fv fragments or single chain Fv molecules and which contain an

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expression-secretion vector comprising a DNA sequence encoding the T7 promoter, a DNA sequence encoding the variable domain of an immunoglobulin heavy chain, a DNA sequence encoding the variable domain of an immunoglobulin light chain, and one or more DNA sequences encoding one or more signal peptide sequences, or which contain an expression-secretion vector comprising a DNA sequence encoding a T7 promoter, a DNA sequence encoding a single chain Fv molecule and a DNA sequence encoding a signal peptide sequence can be identified by one or more of the four general approaches: (a) DNA-DNA hybridization; (b) the presence or absence of marker gene functions; (c) assessing the level of transcription as measured by production of immunoglobulin V_H or V_L chain or single chain Fv molecule mRNA transcripts in the host cells; and (d) detection of the gene product biologically.

In the first approach, the presence of DNA sequences coding for immunoglobulin ${\rm V_H}$ or ${\rm V_L}$ chains or single chain Fv molecules can be detected by DNA-DNA or RNA-DNA hybridization using probes complementary to the DNA sequences.

In the second approach, the recombinant expression-secretion vector host system can be identified and selected based upon the presence or absence of certain marker gene functions (e.g., ampicillin and kanamycin resistance to antibiotics). A marker gene can be placed in the same plasmid as the DNA sequence coding for the immunoglobulin $V_{\rm H}$ or $V_{\rm L}$ chains or single chain FV molecule under the regulation of the same or a different promoter used

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to regulate the immunoglobulin V_H or V_L chain or single chain FV molecule coding sequences. Expression of the marker gene can be used to select for cells harbouring the plasmid containing the DNA sequences coding for the immunoglobulin V_H or V_L chain or single chain FV molecule.

In the third approach, the production of immunoglobulin $V_{\rm H}$ or $V_{\rm L}$ chain or single chain FV molecule mRNA transcripts can be assessed by hybridization assays. For example, total RNA can be isolated and analyzed by Northern blotting or nuclease protection assay using a probe complementary to the RNA sequence.

In the fourth approach, the expression of immunoglobulin $V_{\rm H}$ or $V_{\rm L}$ chains or single chain FV molecules can be assessed biologically, for example, by Western blotting or binding to antigen, or by sequencing of the protein product.

Once an expression-secretion vector has been introduced into an appropriate host cell, the host 20 cell may be cultured under conditions permitting expression of large amounts of Fv fragments or single chain Fv molecules. Such Fv fragments or single chain Fv molecules may be used in the same manner as the full length antibody molecules from 25 which they are derived. For example, they may be used for in vivo and in vitro immunological diagnostic procedures, and may be used therapeutically, either alone or after conjugation to drugs and toxins. They may also be used for 30 structural studies, for example, using nuclear magnetic resonance (NMR) and X-ray crystallography.

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If desired, the Fv fragments or single chain Fv molecules produced in this manner may be isolated and purified to some degree using various protein purification techniques. For example, chromatographic procedures such as ion exchange chromatography, gel filtration chromatography and immunoaffinity chromatography may be employed.

The DNA sequences of expression-secretion vectors, plasmids or DNA molecules of the present invention may be determined by various methods known in the art. For example, the dideoxy chain termination method as described in Sanger et al., Proc. Natl. Acad. Sci. USA 74, 5463-5467 (1977), or the Maxam- Gilbert method as described in Proc. Natl. Acad. Sci. USA 74, 560-564 (1977) may be employed.

It should be understood that the methodology described herein can be used to prepare Fv fragments or single chain Fv molecules derived from animal species other than mice, and Fv fragments or single chain Fv molecules for a wide variety of different antigens, for example, digoxin and fibrin. It should also be understood that the methodology described herein can be used in the production of modified Fv fragments or single chain Fv molecules. In this case, the DNA sequences coding for the variable domain of the immunoglobulin heavy chain, or the variable domain of the immunoglobulin light chain, or both, or for the single chain Fv molecule, can be modified (i.e., mutated) to prepare various mutations that change the amino acid sequence encoded by the mutated codon. These modified DNA

sequences may be prepared, for example, by mutating the DNA sequences coding for the variable domain of the immunoglobulin heavy chain, or the variable domain of the immunoglobulin light chain, or both, or for the single chain Fv molecule, so that the 5 mutation results in the deletion, substitution, insertion, inversion or addition of one or more amino acids in the encoded polypeptide using various methods known in the art. For example, the methods of site-directed mutagenesis 10 described in Taylor, J. W. et al., Nucl. Acids Res. 13, 8749-8764 (1985) and Kunkel, J. A., Proc. Natl. Acad. Sci. USA 82, 482-492 (1985) may be employed. In addition, kits for site-directed mutagenesis may be purchased from commercial 15 vendors. For example, a kit for performing sitedirected mutagenesis may be purchased from Amersham Corp. (Arlington Heights, IL). Contemplated modifications include, for example, humanization of Fv fragments derived from mice. See, Jones et al., 20 Nature 321, 522 (1986). All such variations are included within the scope of the present invention.

As used above and elsewhere in the present application, the term "modified", when referring to a nucleotide or polypeptide sequence, means a nucleotide or polypeptide sequence which differs from the wild-type sequence found in nature.

The following examples are further illustrative of the present invention. These examples are not intended to limit the scope of the present invention, and provide further understanding of the invention.

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Example 1

Cloning of Genes Encoding Antibody Fragments

Antidigoxin monoclonal antibody 26-10 is a high affinity (5 x 10^9 M- 1) antibody produced against digoxin conjugated to bovine serum albumin (Mudgett-Hunter et al. Mol. Immunol. 22, 477 [1985]). cDNA clones of the genes encoding the ${
m V}_{
m H}$ and ${
m V}_{
m L}$ portions of the 26-10 antibody were made by PCR amplification of cDNA generated by reverse 10 transcription of mRNA isolated from the 2610 hybridoma and sequenced by the dideoxy chain termination method (Figures 1-A [SEQ. ID NO. 1] and 1-B [SEQ. ID NO. 2]). The DNA sequences were compared to genomic 2610 sequences [See, Near, R. I. et al., Mol. Immunol., 27, 901-909 (1990)] to verify that the authentic genes encoding 26-10 had been cloned.

Example 2

Construction of T7 Promoter Based Expression-Secretion Vector

A T7 promoter based expression-secretion vector was made through modification of the pT7-7 plasmid described in Tabor, S. et al., Proc. Natl. Acad. Sci. USA 82, 1074 (1985). The restriction sites in the polylinker region of pT7-7 were altered in such a way that convenient restriction sites were available for cloning DNA fragments containing both 26-10 ${\rm V}_{\mbox{\scriptsize H}}$ and ${\rm V}_{\mbox{\scriptsize L}}$ and their respective signal sequences (Figure 2 [SEQ. ID NO. 3 and SEQ. ID NO. 4]) on the same plasmid as an artificial operon. The signal sequences, ompA (Movva et al., J. Biol. Chem. <u>255</u>, 27 [1980]) and

phoA (Inouye et al., J. Bacteriol. 149, 434 [1982]) were engineered such that novel restriction sites were generated without changing the amino acid sequence of the signal peptides. Hence, correct processing would be expected to generate the authentic N-terminal sequences of both chains and for the proteins to be secreted into the periplasmic space. These modified signal sequences were made by PCR using E. coli chromosomal DNA as template.

For ompA, the following oligonucleotides were used as PCR primers:

5' Primer

- 5'-AACATATGAAAAAGACAGCTATCGCCATT-3' [SEQ. ID NO. 5]
 3' Primer
- 15 5'-GAATTCGGCCTGCGCAACGGTCGCGAAACCAGCTAGCGCCACTGC-3'
 [SEQ. ID NO. 6].
 For phoat the following oligonucleotides were used

For phoA, the following oligonucleotides were used as PCR primers:

5' Primer

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- 20 5'-AACATATGAAACAAAGCACTATTGCACTGGCA-3' [SEQ. ID NO. 7]
 3' Primer
 - 5'-GAATTCGGCCTTGGTCACCGGGGTAAACAGTAA-3' [SEQ. ID NO. 8]
 The modified signal sequences are shown in Figure
 2 [SEQ. ID NO. 3 AND SEQ. ID NO. 4]. In both
- 25 cases, and for all PCR procedures, PCR was performed using a GeneAmp Kit (Perkin-Elmer Cetus, Norwalk, CT) as recommended by the manufacturer.

The initial step in the construction of the expression-secretion vector was the previously mentioned modification of the pT7-7 polylinker region.

In order to generate a plasmid containing the 26-10 $\rm V_{H}$ region (see Figure 3A), the pT7-7

plasmid was cut with BamH1 and Sall, then filled in with Klenow to effectively destroy the BamH1, Sall and Xbal sites in the pT7-7 polylinker. resulting vector was then cut with Xbal and filled in with Klenow to destroy the Xbal site upstream of the ribosome binding site. This plasmid was then cut with Smal and ligated using T4 DNA ligase with an Xbal linker to generate the pT7-11 vector. The pT7-11 plasmid was cut with Ndel and EcoR1 and ligated using T4 DNA ligase with an Ndel/EcoR1 10 fragment containing the ompA signal sequence, to generate the pT7-11 OmpA vector. The pT7-11 OmpA plasmid was then cut the Nrul and EcoRl and ligated using T4 DNA ligase in frame with a fragment encoding the $V_{\mbox{\scriptsize H}}$ chain of 2610 generated by PCR 15 using as template mRNA isolated from the 2610 hybridoma and the following oligonucleotide primers: 5' Primer

5'- AACATATGTTCGCGACCGTAGCGCAGGCCGAGGTCCAGCTGCAACAGTCCGGA-3'
[SEQ. ID NO. 9]

3' Primer

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5'- TTGAATTCTTATTATGAGGAGACGGTGACTGAGGCTCC-3'
[SEQ. ID NO. 10]

Oligonucleotides used for the amplification generated Nrul and EcoRl sites at the 5' and 3' ends, respectively, of the amplified $V_{\rm H}$ fragment. The resulting plasmid was designated $V_{\rm H}^{\rm pD}$.

In order to generate a plasmid containing the 26-10 $\rm V_L$ region (see Figure 3B), the phoA signal sequence was PCR amplified and cloned as a Ndel/EcoRl fragment into unmodified pT7-7. The 26-10 $\rm V_L$ DNA was amplified by PCR using the oligonucleotide primers indicated below to generate

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a fragment suitable for cloning into the pT7phoA expression-secretion vector:

5' Primer

5'-AACATATGACCAAGGCCGATGTTGTGATGACCCAAACTCCA-3'
[SEQ. ID NO. 11]

3' Primer

5'-TTCTGCAGTTATTACCGTTTGATTTCCAGCTTGGTGCC-3'
[SEQ. ID NO. 12]

The amplified 26-10 $\rm V_L$ fragment was cut with Styl and ligated using T4 DNA ligase with the pT7phoA plasmid which had been cut with Styl and Smal, resulting in the ligation of the 26-10 $\rm V_L$ as a Styl/blunt ended fragment. The resulting plasmid was designated $\rm V_L pD$.

The $V_L pD$ plasmid was then cut with BamH1 and Sall, filled in with Klenow and religated with T4 DNA ligase to generate plasmid $V_L pD$ -Xbal (Figure 3C).

The $V_H^{\rm pD}$ and $V_L^{\rm pD-Xbal}$ plasmids were then used to construct the FvpD expression-secretion vector. The $V_L^{\rm pD-Xbal}$ plasmid was cut with Xbal and Hindlll to release the light chain containing the signal peptide sequence but lacking the T7 promoter sequence. This fragment was then ligated using T4 DNA ligase with Xbal/Hindlll cut $V_H^{\rm pD}$ to yield FvpD (Figure 3D).

The final construct (FvpD) as well as the intermediate constructs were sequenced by dideoxy DNA sequencing to assure no alterations affecting amino acid sequences had occurred during their construction/amplification.

Example 3

Expression of 26-10 Fv from Plasmid FvPD

To express 26-10 Fv from FvpD, a second compatible plasmid called Gp1-2 (Tabor et al., supra), which contains the T7 RNA polymerase gene 5 under the control of the temperature sensitive lambda cI repressor and the kanamycin resistance gene, was co-transformed as described in Maniatis et al., supra. with FvpD into MC1061 E. coli cells using selection for both ampicillin and kanamycin 10 resistant transformants. MC1061 cells may be obtained from Clontech (Palo Alto, CA) or the American Type Culture Collection (Rockville, MD). The transformants were inoculated into 2 x YT medium containing 20 μ g/ml kanamycin and 50 μ g/ml 15 ampicillin, and grown at 25°C to $OD_{600} = 2.0$ prior to induction of 26-10 Fv. When the cells containing the Gp1-2 plasmid are shifted to 42°C for thirty minutes this inactivates the temperature sensitive repressor protein and permits expression of the T7 20 RNA polymerase gene. The T7 RNA polymerase protein is then able to promote transcription of the 26-10 $\rm V_{H}$ and $\rm V_{I,}$ genes by utilizing the T7 promoter present upstream of the two genes. The cells were then shifted to 25°C for 30 minutes 25 to facilitate the proper processing and assembly of the $V_{\overline{H}}$ and $V_{\overline{L}}$ polypeptides. As shown in Figure 4 (lane 7), temperature induced cells containing both the Gp1-2 and FvpD plasmids expressed two polypeptides that migrated with apparent molecular 30 weights of 12 kd and 15 kd. The size of the 12 kd polypeptide was essentially identical to the size of the 26-10 $V_{\text{T.}}$ chain (12.2 kd) predicted from the

polypeptide encoded by the 26-10 V_{Γ} DNA sequence. The 15 kd polypeptide appeared to migrate slower than the predicted size (13.2 kd) of the polypeptide encoded by the 26-10 V_{H} DNA sequence. These two polypeptides also appeared to be properly localized as they were found to be greatly enriched in the periplasmic fraction. The 26-10 Fv was purified by affinity chromatography of the periplasmic fraction on a ouabain-Sepharose affinity column (ouabain is a digoxin congener). 10 The periplasmic fraction was harvested by osmotic shock as described in Skerra et al., Science 240, 1038 (1988). All steps were performed on ice or at 4°C. After induction, the cells from a 1 liter culture were harvested by centrifugation at 4000 x 15 g for 10 minutes. The cell pellet was suspended in 10 ml of TES buffer (0.2 M Tris HCl pH 8.0, 0.5 mM EDTA, 0.5 M sucrose). The suspended cells were then subjected to osmotic shock by the addition of 15 mls of diluted TES (TES diluted 1:4 with H_2O) to 20 release the proteins present in the periplasmic space. After a 30 minute incubation on ice, the cells were removed by successive centrifugations of 5000 x g for 10 minutes and 38,000 g for 15 minutes. The supernatant containing the periplasmic fraction 25 was then subjected to affinity chromatography. Upon elution of the bound material with 20 mM ouabain, fractions 3 and 4 (Figure 4, lanes 1 and 2) revealed two polypeptides of the correct size that were selectively purified. The following 30 evidence indicated that this is 26-10 Fv: (1) It competed with 125 I-26-10 whole antibody in competitive RIA assays; (2) It bound 125I-digoxin

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with K_A=1.3 x 10⁹ M⁻¹ compared to 5 x 10⁹ M⁻¹ for 26-10 whole antibody; (3) N-terminal sequencing of V_L and V_H variable domains indicated correct processing and expected N-terminal sequences. The yield of purified Fv was demonstrated to be 1 mg/L. It should be possible to further improve the yield by using protease deficient strains as host, by optimizing fermentation conditions, by using alternative signal sequences, and by co-expressing enzymes and chaperones (e.g., heavy chain binding protein [BIP]) that are normally employed for immunoglobulin chain assembly in mammalian cells.

The 26-10 Fv made by this method is stable for at least a two months, and probably longer, when stored at 4°C at nM range protein concentrations.

Example 4

Alternate Expression of 26-10 Fv from FvpD

A second method was also used to express 26-10 Fv from FvpD. In this method, the FvpD plasmid was transformed into E. coli strain JM109/DE3 [Promega; See also, Studier, F.W. et al., Methods in Enzymology 185, 60-88 (ed. D.V. Goeddel) Academic Press (1990)]. JM109/DE3 contains an integrated copy of the T7 RNA polymerase gene under the control of a lac promoter. JM109/DE3 cells harboring the FvpD plasmid were grown until the A600nm of the cells measured between 1.0 and 2.4 in modified 2 x YT medium (2% bacto tryptone, 1% yeast extract, 0.5% sodium chloride, 0.2% glycerol, 50 mM potassium phosphate pH 7.2) with glucose (0.4%), ampicillin (50 mg/liter) at 37°C. The cells were then cooled to 24°C. Subsequently, isopropyl

beta-D-thiogalactoside (IPTG) was added to a final concentration of 0.05 mM to induce transcription of the T7 RNA polymerase gene. After the addition of IPTG, the cells were allowed to incubate at 24°C for 16 hours, and screened for periplasimic proteins.

It was found that osmotic shock supernatants (the periplasmic fractions from IPTG-treated JM109/DE3 cells containing the FvpD plasmid) contained two proteins that comigrated with 10 proteins found in heat-treated MC1061/Gp1-2 cells. These two polypeptides appeared to be greatly enriched in the osmotic shock supernatant. When 26-10 Fv was purified from the osmotic shock supernatant using a ouabain-Sepharose 15 column (see Example 3), two polypeptides were isolated of the approximate sizes expected for the 26-10 V_H and V_L chains (15 and 12 kD). The yield of affinity purified 26-10 Fv from the JM109/DE3 strain was 14 mg/liter. In the 20 JM109/DE3 strain, the maximum level of 26-10 Fv accumulation was observed approximately 16 hours after induction, while in MC1061/GP1-2 (Example 3), the maximum level of 26-10 Fv accumulation occurred one hour after the start of induction. 25 . Coomassie staining of protein fractions separated by SDS-PAGE indicated that in both JM109/DE3 and MC1061/Gp1-2 (Example 3), most of the 26-10 Fv protein was found in the periplasm. N-terminal protein sequence analysis of the JM109/DE3 produced 30 protein revealed that both the $V_{\rm H}$ (approximately 15 kD) and $V_{T.}$ (12 kD) chains had been correctly processed by the bacterial export system. In both

the JM109/DE3 and MC1061/Gp1-2 (Example 3) strains, it was necessary to cool the cells to 25°C after the protein inductions. Incubation at temperatures exceeding 27°C resulted in the accumulation of proteins of approximately 17 kD and 12 kD that did not bind to the ouabain-Sepharose column.

Example 5

Expression of Biologically Active Single Chain Fv The expression systems of the present

invention were also used to express biologically active single chain Fv (sFv) molecules.

The sFv form of the 26-10 antibody was constructed by PCR amplification with mutagenic oligonucleotides to create novel restriction sites 15 (and to insert sequences encoding a peptide linker between the two chains.) Briefly, as summarized in Figure 5, the genes encoding the variable regions of the light (V_L) and heavy (V_H) chains were separately PCR amplified under the conditions 20 described in Example 2 using as a template the cDNA clones of the genes encoding the ${
m V}_{
m H}$ and ${
m V}_{
m L}$ portions of the 26-10 antibody (see Example 1) and the following oligonucleotide primers:

3' V_L 26-10 Sequence Overlap Extension (SOE) 25 5'-AGAGCCGGATCCACCGGAACCGGAGCCGCCAGAACCAGAACCACCCCGTTTGATTTC CAGCTTGGT-3'

[SEQ. ID NO. 13]

5' V 26-10 BstE2 (for PhoA pT7)

5'-CCATCGGTGACCAAAGCCGATGTTGTGATGACCCAAACT-3' 30

[SEQ. ID NO. 14]

5' VH 26-10 SOE

5'-GTGGTTCTGGTTCTGGCGGCTCCGGTTCCGGTGGATCCGGCTCTGAGGTCCAGCTG CAACAGTCC-3'

[SEQ. ID NO. 15] 35

15

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3' V_H 26-10 Sall 5'-CCCGTCGACCTGCAGGCATGCGGATCCTTATGAGGAGACGGTGACTGAGGCTCC-3' [SEQ. ID NO. 16]

These oligonucleotides had complementary sequences, and included sequences encoding the peptide linker engineered between the V_L and V_H chains, so that the V_L and V_H sequences could later, after a second round of PCR amplification, form a complete double stranded DNA molecule encoding a single chain Fv molecule containing a 15 amino acid linker with the following sequence:

-Gly-Gly-Ser-G

[SEQ. ID NO. 17]

This DNA construct was designated PCR amplified 26-10 sfv. The PCR amplified 26-10 fv and the plasmid designated pT7PhoA (See Example 2) were both cut with the restriction enzymes BstE2 and Sall and ligated, resulting in the plasmid designated pT7PhoA26-10sfv. This plasmid encodes a single chain protein with the following domains (going from the N-terminus to the C-terminus: PhoA leader - 26-10 variable light chain- linker- 26-10 variable heavy chain) (See Figure 6 [SEQ. ID NO. 18] for the DNA and encoded amino acids sequences of this construct).

The pT7PhoA26-10sFv plasmid was transformed by the CaCl₂ method (See, Maniatis et al., supra) into E. coli strain BL21/DE3/pLysS [See, Studier, F.W. et al., Methods in Enzymology 185, 60-88 (ed. D.V. Goeddel) Academic Press (1990)]. Cells harboring the pT7PhoA26-10sFv plasmid were grown overnight in Minimal Medium (7.6 mM NH₄SO₄,

11.0 mM sodium acetate, 12.7 mM succinic acid, 60.3 mM K_2HPO_4 , 68 μ M $CaCl_2.2H_2O$, 35 μ M $ZnSO_4.7H_2O$, 59 μ M MnSO $_4$. H_2 O, 741 μ M thiamin, 2032 μ M niacin, 12 μ M biotin, 40 μ M FeCl₃.6H₂O, 3 μ mM Na₂MoO₄.2H₂O, 3 μ M $\text{Cuso}_4.5\text{H}_2\text{O}$, 3 μM H_3BO_3 , 3 μM vitamin B-12, 4 mM $MgSO_4$, 22 mM glucose, 50 μ g/ml ampicillin, 20 μ g/ml chloramphenicol) at 37°C, then diluted 1:20 into 2 x YT medium (as in Example 4) at 37° C and grown until the A_{600nm} of the cells measured between The cells were then cooled to 24°C. 0.5 and 1.0. 10 Subsequently IPTG was added to a final concentration of 0.2 mM to induce transcription of the T7 RNA polymerase gene. After the addition of IPTG the cells were allowed to incubate at 24°C for 16 hours and screened for periplasmic proteins and 15 proteins in the culture supernatant. Under these conditions, a yield of 3 to 10 mg of affinity purified 26-10 sFv protein per liter cell culture was obtained. The affinity purified material had a molecular weight of about 29 kd, as shown by 20 SDS-PAGE, which is in good agreement with the theoretically predicted molecular weight of about 26 kD. The fact the 26-10 sFv protein is biologically active was shown by its ability to bind to and be purified using a ouabain-Sepharose 25 affinity column (see Example 3).

All publications and patents referred to in the present application are incorporated herein by reference to the same extent as if each individual publication or patent was specifically and individually indicated to be incorporated by reference.

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SEQUENCE LISTING

- (1) GENERAL INFORMATION:
 - APPLICANTS: Ng, Shi Chung; Anthony, (i) James G.; Wong, Sui-Lam
 - TITLE OF THE INVENTION: Expression-(ii) Secretion Vectors for the Production of Biologically Active Fv Fragments
 - (iii) NUMBER OF SEQUENCES: 12
 - (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Burton Rodney Squibb . Corporation
 - P.O. Box 4000 (B) STREET:
 - Princeton (C) CITY:
 - New Jersey (D) STATE:
 - USA (E) COUNTRY:
 - 08543-4000 (F) ZIP:
- INFORMATION FOR SEQ. ID NO.: 1 (2)

(A) LENGTH:

- SEQUENCE CHARACTERISTICS: (i)
 - 357 base pairs
 - nucleic acid (B) TYPE:
 - (C) STRANDEDNESS: double stranded
 - linear (D) TOPOLOGY:

-28-

(xi) SEQUENCE DESCRIPTION: SEQ. ID NO.:1

Glu	Val	GIN	ren	5		TCC Ser	_		10							48
Ser	Val	Arg	Met	SCL	0,10	AAG Lys		25					30			96
Tyr	Met	ASI	TGG Trp	A G T	5	CAG Gln	40					43				
Gly	Tyr	ATT Ile	Ser	FIO	~1~	AGT Ser 55	_				60					
Lys	GGC Gly	AAG Lys	HIG	1111	70	ACT Thr				75)				•	
Met	Glu	i Let	1 WIG	305		G ACA			90)				,-		
GCA Ala	GG/	A TC	G TC0 r Se:		AA!	r AAC n Lys	TGC TI	GCT Ala	T ATO	GA(As)	TAC TY	TGC TI	GGI Gly 110	CAC His	GGA Gly	
GC0 Ala	C TC a Se	A GT r Va 11	1 Tn	C GT(C TC 1 Se	C TC	A									357

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	(2)	(i	(A (B (C (D	QUENC) LEI) TYI) STI) TOI	CE CI NGTH PE: RAND POLO	HARAC : EDNE: GY :	SS:	ISTICS: 339 base pairs nucleic acid double stranded linear									
	(xi) SEQUENCE DESCRIPTION: SEQ. ID NO.: 2 GAT GTT GTG ATG ACC CAA ACT CCA CTC TCC CTG CCT GTC AGT CTT GGA 48																
GAT Asp 1	GTT Val	GTG Val	ATG Met	ACC Thr 5	CAA Gln	ACT Thr	CCA Pro	CTC Leu	TCC Ser 10	CTG Leu	CCT Pro	GTC Val	AGT Ser	CTT Leu 15	GGA Gly	48	
Asp	Gln	Ala	TCC Ser 20	He	Ser	cys	ALG	25	501				30				
Asn	Gly	Asn 35	ACC Thr	Tyr	Leu	ASI	40	171	Dea	01	-1-	45	-				
CCA Pro	AAG Lys 50	CTC Leu	CTG Leu	ATC Ile	TAC Tyr	AAA Lys 55	GTT Val	TCC Ser	AAC Asn	CGA Arg	TTT Phe 60	TCT Ser	GGG	GTC Val	CCA Pro	192	
Asp 65	Arg	Phe	AGT Ser	GIY	70	GTY	. ser	GIJ	1.12	75					80		
AGC Ser	AGA Arg	Val	GAG Glu	A1a 85	GIU	Asp	Leu	GIJ	90	-1-		-		95			
ACA Thr	CAT His	GTI Val	CCI Pro	Pro	ACG Thr	TTC Phe	GGI	GGA Gly 105	0-1	ACC Thr	AAG Lys	CTG	GAA Glu 110	ATC	AAA Lys	336	
CGC		•														339	

	INFORMATION FOR SEQ. ID NO.: 3 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 68 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double stranded (D) TOPOLOGY: circular	
	(xi) SEQUENCE DESCRIPTION: SEQ. ID NO.: 3	
AACAT	ATG AAA AAG ACA GCT ATC GCC ATT GCA GIG GCG CIA GGT GCA GGT GCA GIG GCG CIA GGT GCA GGT GCA GIG GCG CIA GGT GCA GGT GC	47
TTC GC Phe Al	CG ACC GTT GCG CAG GCC La Thr Val Ala Gln Ala 20	68
(2)	INFORMATION FOR SEQ. ID NO.: 4 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 68 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double stranded (D) TOPOLOGY: circular	
	(xi) SEQUENCE DESCRIPTION: SEQ. ID NO.: 4	
AACAT	ATG AAA CAA AGC ACT ATT GCA CTG GCA CTC TTA CCG TTA CTG Met Lys Gln Ser Thr Ile Ala Leu Ala Leu Leu Pro Leu Leu 1 5	47
TTT A Phe T 15	CC CCG GTG ACC AAG GCC Thr Pro Val Thr Lys Ala 20	68
(2)	INFORMATION FOR SEQ. ID NO.: 5 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 29 bases (B) TYPE: nucleic acid (C) STRANDEDNESS: single stranded (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ. ID NO.: 5	
ממ	CATATGAA AAAGACAGCT ATCGCCATT	29

(2)	(i) S (ATION FOR SEQ. 1D NO.: 6 EQUENCE CHARACTERISTICS: A) LENGTH: 45 bases B) TYPE: nucleic acid C) STRANDEDNESS: single stranded (D) TOPOLOGY: linear	
		SEQUENCE DESCRIPTION: SEQ. ID NO.: 6	
GAATT	CGGCC :	TGCGCAACGG TCGCGAAACC AGCTAGCGCC ACTGC	45
(2)	(i)	MATION FOR SEQ. ID NO.: 7 SEQUENCE CHARACTERISTICS: (A) LENGTH: 32 bases (B) TYPE: nucleic acid (C) STRANDEDNESS: single stranded (D) TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ. ID NO.: 7	
AACAT		ACAAAGCACT ATTGCACTGG CA	32
(2)		MATION FOR SEQ. ID NO.: 8 SEQUENCE CHARACTERISTICS: (A) LENGTH: 33 bases (B) TYPE: nucleic acid (C) STRANDEDNESS: single stranded (D) TOPOLOGY: linear	
	(xi)	SEQUENCE DESCRIPTION: SEQ. ID NO.: 8	
GAAT.	rcggcc	TTGGTCACCG GGGTAAACAG TAA	33
(2)	INFOI (i)	RMATION FOR SEQ. ID NO.: 9 SEQUENCE CHARACTERISTICS: (A) LENGTH: 53 bases (B) TYPE: nucleic acid (C) STRANDEDNESS: single stranded (D) TOPOLOGY: linear	
		SEQUENCE DESCRIPTION: SEQ. ID NO.: 9	
AACA	TATGTT	CGCGACCGTA GCGCAGGCCG AGGTCCAGCT GCAACAGTCC GGA	53

(1) S. (1) (1) (1) (1) (1) (1) (1) (1) (1) (1)	ATION FOR SEQ. ID NO.: 10 EQUENCE CHARACTERISTICS: A) LENGTH: 38 bases B) TYPE: nucleic acid C) STRANDEDNESS: single stranded D) TOPOLOGY: linear	
(xi) S	SEQUENCE DESCRIPTION: SEQ. ID NO.: 10	38
	ATTATGAGGA GACGGTGACT GAGGCTCC	
(i) S	MATION FOR SEQ. ID NO.: 11 SEQUENCE CHARACTERISTICS: (A) LENGTH: 41 bases (B) TYPE: nucleic acid (C) STRANDEDNESS: single stranded (D) TOPOLOGY: linear	
(xi)	SEQUENCE DESCRIPTION: SEQ. ID NO.: 11	41
AACATATGAC	CAAGGCCGAT GTTGTGATGA CCCAAACTCC A	12
(1)	(A) LENGTH: nucleic acid (B) TYPE: nucleic acid (C) STRANDEDNESS: single stranded (D) TOPOLOGY: linear	
	SEQUENCE DESCRIPTION: SEQ. ID NO.: 12 ATTACCGTTT GATTTCCAGC TTGGTGCC	38

What is Claimed is:

- 1. An expression-secretion vector capable of producing a biologically active single chain Fv molecule comprising a DNA sequence encoding the T7 promoter, a DNA sequence encoding a single chain Fv molecule, and a DNA sequence encoding a signal peptide sequence.
- 2. The expression-secretion vector according to Claim 1 wherein the signal peptide sequence is phoA.
- 3. A host cell comprising an expressionsecretion vector according to Claims 1 or 2.
 - 4. The host cell according to Claim 3 wherein the host cell contains a stably integrated copy of the T7 RNA polymerase gene.
- 5. The host cell according to Claim 4 wherein the host cell is *E. coli* strain JM109/DE3 or *E. coli* strain BL21/DE3/pLysS.
- 6. A method for producing a biologically active single chain Fv molecule comprising culturing a host cell according to Claim 3 under conditions permitting expression of the biologically active single chain Fv molecule.

FIGURE 1-A

1					AAC	B S B H E E s Aa p g Cc CBcS C pM vu uD iAvo M vsoc HvM Ms a9 1d Eli5 w iaRr pin Ip I6 Oe IuJ7 o JJIF hJ1 II II II IIII I IIII III / / / / // CAGTCCGGACCTGAACTGGTGAAGCCTGGGGCTTCAGTG GTCAGGCCTGGACTTGACCACTTCGGACCCCGAAGTCAC											60							
														M										
	E	V	¥		¥	×		•	•	_	_	•	-						_					
	-													N 1					S t	СВ				
	BM		E-											a			В		_	vs				
	bb vo		F											Ī			s			ia				
	II		k											Ī			r		T	JJ				
	ΪΪ		Ï											I			I		I	II				
	/																							
	TCC	rgC2	AAG:	rcT?	CTC	GAT	CAC	ATA	rtc.	ACTO	AC.	rrc:	rac.	ATG	AAC:	rgg	GTG	AGG	GCAGAGC + 120					
61				+																	120			
	AGG	ACG:	rtc	AGA!	AGA	CCTA	\TG	TAT	AAG'	rgac	TG	AAG	A'I'G'	TAC:	TTG	ACC	CAC	.1	GIC.	LCG				
	s	С	ĸ	s	s	G	Y	I	F	T	D	F	Y	M	N	W	v	R	Q	s				
																34	,							
		N		_												M a			C					
		1		С												e			vB					
	DNS			v i													I is							
	sct			Ĵ												Ī			Jr					
		oyI J III I															•		II	II				
	111			_																				
	CAT	GGA	AAG	AGC	CTT	GAT	TAC	ATT	GGA	TAT	TT	TCT	CCT	TAC	AGT	GGI	GTI	CACI	'GGC	TAC				
121				+			-+-			+-				+			+-			+	180			
	GTA	CCT	TTC	TCG	GAA	CTA	ATG	TAA	CCT	ATA:	raa	AGA	GGA	ATG	TCA	CCA	CAA	YTGA	CCG	ATG				
	н	G	K	s	L	D	Y	I	G	Y	I	s	P	Y	s	G	V	T	G	Y				
								H											С					
								C a		_	s	A						N	ر الا					
																			ni					
	iaI sfc ni JeI uec 1J																							
								TTT		Ī	T	Ī						1	ΙI					
								11																
•	AAC	CAG	AAG	TTC	AAG	GGC	AAC	GCC	ACA	TTG	ACI	GTA	GAC	CAAC	TCC	TC	CAG	CAC	AGCC	TAC				
181							-+-			+				-+			+-				240			
	TTG	GTC	TTC	AAG	TTC	CCG	TTC	CCGG	TGI	TAAC	TGA	CAI	CTC	TTC	:AGG	AG)C'(.'T'G	LCGG	ATG				
	N	Q	ĸ	F	K	G	K	Α	T	L	T	V	D	K	s	s	s	Т	A	Y				
		_																						

FIGURE 1-A (continued)

	N 1 a I I I	Av 1: u.: II	/a2c	F I n JSuS Lp4s LiHt IIII // /	v i J	M n 1 I	AÇA'	B b v I		H iT nf fi II	S f e I	P s t I	GTCT	'AT'	rac'	TGT(GCA(S p A n I I	TCG	A 1 w I	300
241	TACC	TC	GAG	 3CG1	CG	GAC	TGT.	AGC	CTC	CTA	AGA	CGT	CAG								300
	М	E	L	R	s	L	Т	s	E	D	s	A	v	Y	Y	С	A	G	s	s	
										МT]	МТ						
				(2				as			CN Eas			as	E					
				B	7					Вер		Hv1D sep piad pI4 hJIe 3I5 IIVI III			_	M		s			
				C						sI4						ņ		m			
				g.						rI5					l I		A				
				I						III		1	IVI	1	<u> </u>	1		_			
	GGG	AT.	AAG'	rgg	SCT.	ATG	GAC	TAC	TGG	GGT	CAC	GGA	GCC?	CA	GTC	ACC	GTC	rcc	TCA	35	7
301	CCCI	rTA'	TTC	ACC	CGA'	TAC	CTG	ATG	ACC	CCA	GTG	CCT	CGG	GT	CAG	TGG	CAG	AGG	AGT		•
	G	N	ĸ	W	A	M	D	Y	W	G	Н	G	A	s	v	T	v	s	s		

FIGURE 1-B

																3 A	D p n I		C V i J		
1	GAT			+			-+			+-							-+-	CAA GTT		+	60
	D	v	v	M	T	Q	T	P	L				v	s	L	G	D	Q	A	s	
		M n 1		BB a gsDi 1tp: IYn III:	uM 3a Ae II		Y L T I	C v i J I		R s a I								MD sr ea II	T s p E I	a n I	
61				AGA'	TCT		-+-			+				+			-+-	ATTI TAAA		+	120
	I	s	С	R	s	s	Q	S	L	V	H	s	N	G	N	T	Y	L	N	W	
	N 1RK asp Iar VII / TAC	of ne I	E cP os Nt II	p M I		vB is Jr II	aI eI II // CAG	TCI	s m A I	l u I LAAG	v i J I / CTC	S a u 3 A I	p n I SATC	TAC	:AAA	.GTT	TC:	CAAC	CCGA	TTŢ	100
21							-+-			+				+				GTT			TOO
	Y	L	Q	ĸ	A	G	Q	S	P	K	L	L	I	Y	K	v	S	N	R	F	
	ጥር፣		v1F a0i I9n III	NNPa 11pu aau 1IM VVII ///	M M m S e	CAGO	STT(CAG'	rgg	CAG"	S a u D 3 p A r I I) 1	A 1 W 1	- 7	AGA:	PTT(CAC	:ACT		p n I	;
81				_+			+-							-+				TGA			240
	s	G	v	P	D	R	F	s	G	s	G	S	G	T	D	F	T	L	K	I	

FIGURE 1-B (continued)

241	E c S o t PMy lnL 5lT III / AGCAC			GAG		GAA		CTG		s P E I / TTT	'ATT							CAT			300
		orc R	V	E	A	E.E	D	L			Y	F	С	s	Q	T	т	Н	v	P	
301	M a e I I CCGA	n 1 I .cg'	n l I	+		B a n I	I V CAC	A 1 u I CAAG		+-				2	19						
301	GGÇT	GGCTGCAAGCCACCTCCGTGGTTCGACCTTTAGTTTGCC																			

FIGURE 2A

Omp A:

Nde I

AAICATIATGIAAAIAAGIACAIGCTIATCIGCCIATTIGCAIGTGI

FIGURE 2B

Pho A:

Nde I

AAICATIGTGIAAAICAAIAGCIACTIATTIGCAICTGIGCAICTCITTAICCGITTAI

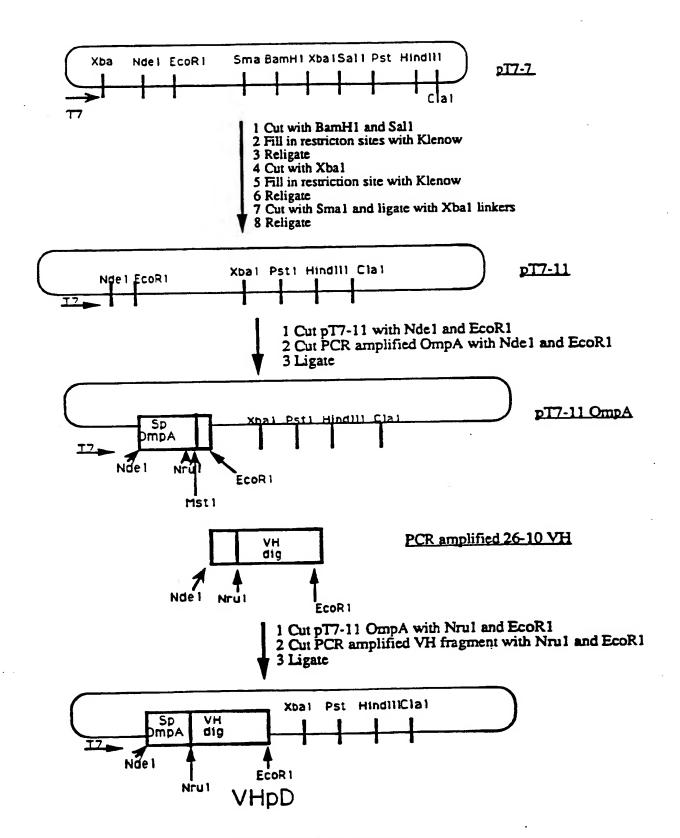
A

BstE II

CTGITTIACCICCTIGTGIACAIAAAIGCC

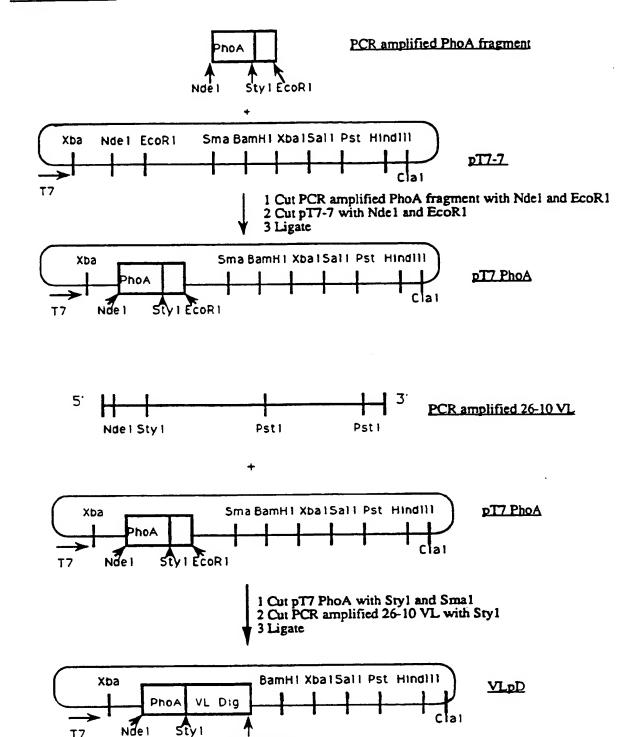
G C G

FIGURE 3-A



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FIGURE 3-B



Blunt/Sma
(Sma site destroyed)

FIGURE 3-C

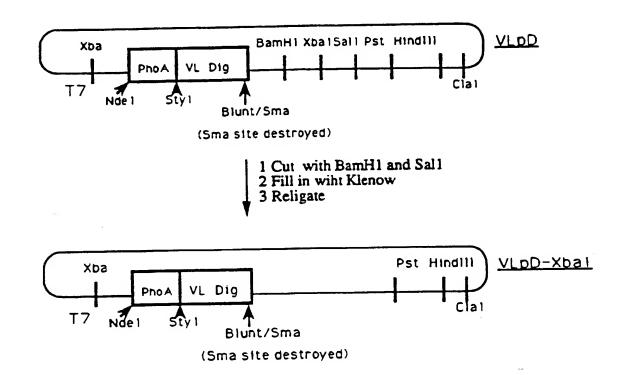
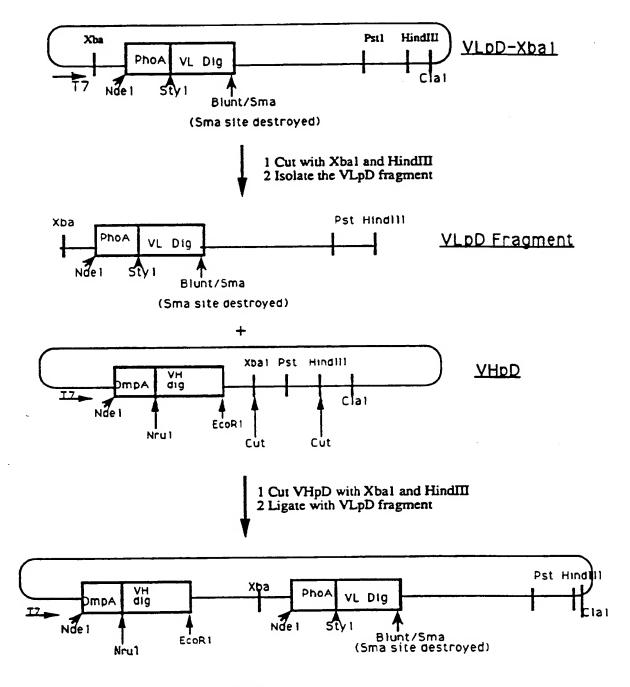


FIGURE 3-D



FVDD

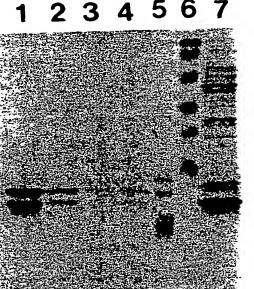
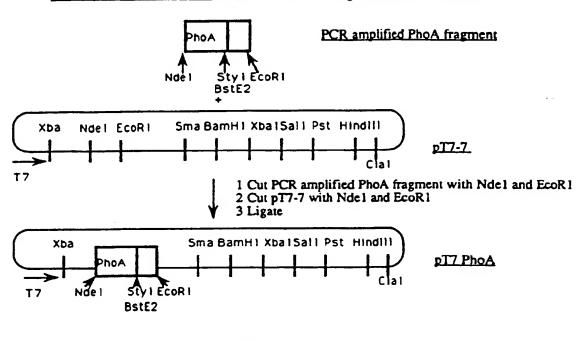
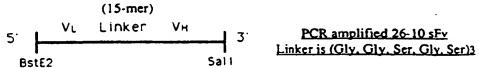


FIG. 4

FIGURE 5

Construction of the 26-10 sFv Expression Vector





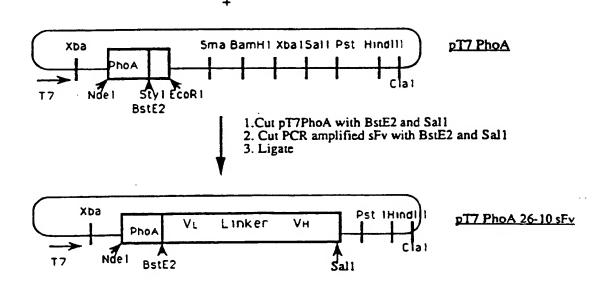


FIGURE 6

(Linear) MAP of:	2610	sFv	from:	1 to:	848
------------------	------	-----	-------	-------	-----

(Linear WAL OI. 20	Nucleotides A	Amino Acids	
phoA signal seq	6-80	1-25	
	81-419	26-138	
26-10 VL seq	420-464	139-153	
Linker seq		154-272	
26-10 VH seq	465-821	DM W	
N d e I	C V B i S R I I I	M BM 1 a B saSs e s MNtecp I a scEIr4 I J pillF5 I I IIIIII / ///	
1	+	L P L L F T P V T	60 (19)
M K Q S S H B aC a S sS uvBeHMNc at 9isIpscr Jy 6J1IhpiF II IIIIIII / //// CCAAGGCCCGGACACC	+	CCCAAACTCCACTCTCCCTGCCTGTCA	120 (39)
K A R T P	EDVVMT	QTPLSLPVS	(33)
s a C u D V 3 P i A n J I I	S C BB a B M v gsDuF c n i ltp3n c l R IYnAa I I I IIII	m i S a J a I I	
GTCTTGGAGATCAAG	CCTCGATCTCTTGCAGAT	CTAGTCAGAGCCTTGTACACAGTAATG	180
L G D Q A	S I S C R S		(59)
MDS srw eaa III	,	H S C a B C a VBHe S AV U D isal m li 3 p Jrel A UJ A n IIII I II I ///	
101	+	CAGGCCAGTCTCCAAAGCTCCTGATCT	
NTYLN	WYLQKA	,	•

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FIGURE 6 (continued)

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E
                           С
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                           0
                                                a
                          AO NNPa
                                                u D
                          v1F11pu M
                                                3 p
                          a0iaau9 m
                                                A n
                          I9nIIM6 e
                          I IIVVII I
                           / ////
    ACAAAGTTTCCAACCGATTTTCTGGGGTCCCAGACAGGTTCAGTGGCAGTGGATCAGGGA
           S N R F S G V P D R F S G S G T (99)
241
                                                    E
                                        S
                 S
                                              MT
                                C
                                     BB a
                                     gsDu
                       M
                S u D
                                     1tp3
                                            s op
                                i
                f 3 p
                       n
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                                            i IE
                                J
                                     IYnA
                c A n
                                     IIII
                                            I II
    301
      D F T L K I S R V E A E D L G I Y F C S (119)
                 N
             Α
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                                           AVM
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                 Is
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I III
                                   n I
             I
                 Ιp
                                           III
                 II
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    CTCAAACTACACATGTTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAAATCAAACGGG
      Q T T H V P P T F G G G T K L E I K R G (139)
361
                                                     F N
                                      S
                   F
                                                    CnCsP
                                 BB N a C
                   n CN
                           N
                                 asD1MMuBAvD
                                                   Avuvpv
                   u vlBM
                           1BAM
               Α
                                 mtpans3blid
                                               s
                                                   li4iBu
                   4 iaes
                           aels
               C
                                                   uJHRII
                                               a
                                 HYnIlpAvwJe
                   H JItp
                           Itwp
               i
                                                   IIIIII
                                 IIIVIIIII
                   I IVII
                           VIII
                                                    11 11
                                 / / // /
     gtggttctggttctggcggctccggttccggtggatccggctctGAGGTCCAGCTGCAAC
 421
      G S G S G S G S G S E V Q L Q Q (159)
```

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FIGURE 6 (continued)

```
Ε
            B H E
            p g Cc
                              С
                        CBcS
       В Аа
                             HvM
                        VSOC
            uD iAvo
      BsMvu
                                                    0
            1d Eli5
                        iaRr
                              pin
      epsa9
                        JJIF
                              hJ1
            0e IuJ7
                     0
      tEpI6
                              III
                     I
                        IIII
            II I II
      IIIII
    AGTCCGGACCTGAACTGGTGAAGCCTGGGGCTTCAGTGAGGATGTCCTGCAAGTCTTCTG
      S G P E L V K P G A S V R M S C K S S G (179)
481
                      Т
                                               N
                           N
                                           CB
                                               1
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                      đ
                                           vsDHNaS
                                  В
                           aM
                                           iaspcIt
                           In
                      I
                                           JJaholy
                           I1
                                  r
                                           IIIIIII
                           II
    GATACATATTCACTGACTTCTACATGAACTGGGTGAGGCAGAGCCATGGAAAGAGCCTTG
         I F T D F Y M N W V R Q S H G K S L D (199)
541
                                 М
                                         С
                                 а
                                         VΒ
                            В
                                 е
                                         is
                                 Ι
                             s
                                         Jr
                                 Ι
                             1
                                         II
     ATTACATTGGATATATTTCTCCTTACAGTGGTGTTACTGGCTACAACCAGAAGTTCAAGG
601
      Y I G Y I S P Y S G V T G Y N Q K F K G (219)
                                                     В
                                                        F
                                                     р
           Н
                                                   CB1 Hn C
                                        С
          C a
                                                 Ava2AguSv
                                       Mv
          vHe
                 G S
                                                  1in8ci4si
                                       ni
                 s f
                     C
          iaI
                                                  uJI6iAHtJ
                                       IJ
                     С
          JeI
                 u e
                                                  IIIIIIII
          III
     GCAAGGCCACATTGACTGTAGACAAGTCCTCCAGCACAGCCTACATGGAGCTCCGCAGCC
           11
       KATLTVDKSSSTAYMELRSL(239)
```

15/15

FIGURE 6 (continued)

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S
                                                            С
               H
                     C
                                       a
                                                        В
                                                            Bv
                                       u D
                   S V P
        ВВ
                iT
    M
                                        3 p
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                                                        S
                                                            ci
                   fis
    n
        s b
                nf
                                                        g
                                                            gJ
                   e R t
                                       A n
                fi
    1
         1 v
    I
         I I
                II
                   III
    TGACATCGGAGGATTCTGCAGTCTATTACTGTGCAGGATCGTCGGGGAATAAGTGGGCTA 780
721
       T S E D S A V Y Y C A G S S G N K W A M (259)
                              M T
                                                        S
                                                          N
                 MT
                                                 BB N Ba 1 C asDM1AsuA aNSSV
                                          BE
                         CN
                 as
                              a s
                        Hv1D
                              e p
                                   M
                                          ssA
                Bep
                                                 mtpnacp31 Isfpi
                        piad
                                          mpl
                              I 4
                                    n
                sI4
                                                 HYnlliMAw IpehR
                              I 5
                                    1
                                          MSA
                rI5
                        hJIe
                                                 IIIIVIIII IIIII
                III
                        IVI
                              II
                                    I
                                          III
                                                 1 11 11 1 1
     TGGACTACTGGGGTCACGGAGCCTCAGTCACCGTCTCCTCAtaaggatccgcatgcctgc
781
        Y W G H G A S V T V S S *
      S
      s
      e
      8
     P3
         s
         a
     t7
         1
         I
     II
     aggtcgac
841
     ---- 848
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INTERNATIONAL SEARCH REPORT

International application No.
PCT/US92/08881

IPC(5)	SSIFICATION OF SUBJECT MATTER :C12P 21/06 :435/69.6									
According to International Patent Classification (IPC) or to both national classification and IPC										
B. FIELDS SEARCHED										
Minimum d	ocumentation searched (classification system followe	d by classification symbols)								
U.S. :	NONE									
Documental	tion searched other than minimum documentation to th	e extent that such documents are included	in the fields searched							
none										
Electronic o	data base consulted during the international search (na	ame of data base and, where practicable,	, search terms used)							
APS, Dia	log, "single chain Fv" "T7 promoter" "phoA" "singl	e peptide sequence"								
C. DOC	CUMENTS CONSIDERED TO BE RELEVANT									
Category*	Citation of document, with indication, where a	ppropriate, of the relevant passages	Relevant to claim No.							
Y	Proceedings of the National Academy of Sciences, vet al., "A bacteriophage T7 RNA polymerase/procexpression of specific genes", pages 1074-1078, se	4								
Y	Science, volume 240, issued 20 May 1988, Ske immunoglobulin Fv fragment in Escherichia coli",	1-6								
Y	Methods in Enzymology, volume 185, issued 19 polymerase to direct expression of cloned genes",	1-6								
Y	Science, volume 242, issued 21 October, 1988, Bi proteins", pages 423-426, see entire article.	1-6								
Y	Science, volume 240, issued 20 May 1988, Better active chimeric antibody fragment", pages 1041-10	1-6								
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